

STIC-Biotech/ChemLib

75270

From: McGarry, Sean  
Sent: Tuesday, September 10, 2002 9:58 AM  
To: STIC-Biotech/ChemLib  
Subject: SEQ SEARCH

Sean McGarry  
09/917,963  
Office CM1 11D07  
Mail box CM1 11E12  
305-7028

Please, for, 09/917963, an oligomer search of SEQ ID NO:3. Please do NOT search EST data and do not search for interference.  
Thanks

Point of Contact:  
Toby Port  
Technical Info. Specialist  
CM1 6A04  
703-308-3534

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 9/10/02  
Searcher Prep/Review \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: 1  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_









```

Source
1. 3224
/organism "Homo sapiens"
/db_xref "taxon:9606"
/feature_type "liver"
/clone_lib "Stratagene human liver cDNA"
gene
87..2271
/anne "MIP"
87..2271
/anne "MIP"
/region_start 1
/product "microsomal triacylglyceride transfer protein"
/feature_id "AA02200.1"
/db_xref "GI:469096"
/definition "MILLAVITTE/PISSY/SAVIGNET/STANDELY/STEVILL/
DROGK/USVOPH/ISSN/VALDM/POD/DOLO/OTIM/DONNE/NOVOC/PEP/EP/
KOR/SIS/IMBEN/EL/PH/IL/LI/HR/KR/PE/SY/NA/VAL/ENI/KOL/AS/PO/L/
SS/IT/NE/VI/SGN/KV/LA/AB/KV/KR/IS/KR/AS/ST/PA/NC/VS/KR/AS/
LYR/LE/SE/VA/LA/EL/HE/NE/NE/LI/KR/IV/SK/RI/ET/EA/PI/MS/KO/AA/
I/RAV/SKY/VA/PI/VG/VE/SG/RO/OSI/ST/MS/ST/RY/OP/NI/SA/VA/SP/AF/TO
HL/KR/KE/IL/LI/KR/KE/VA/POL/VA/VA/SA/OT/SE/AL/DE/DE/SS/IL/LO/ER
FL/AC/ASH/NE/IL/KR/IS/KR/OS/OS/PI/ET/VI/IT/CT/VER/L/ON/RO/KI/KAV
VE/AR/IT/OS/PR/AR/KE/TO/PA/VI/LA/PA/NI/PEG/PL/SL/TA/EA/GE/PI/SH/AT/TA/
Q/RY/DE/PI/DE/VE/K/IN/RY/HL/NE/KR/HE/K/IV/AA/AT/IL/NN/PS/MD/KN/IL/SL/IG
L/JO/BN/KY/MI/AL/VA/UT/RI/PM/PA/RI/IV/PA/RI/PM/VA/NT/PS/SS/SA/VE/PI/EP/
PR/AS/ST/SL/IL/VS/GO/L/PR/EN/NI/FO/IG/KR/IL/OS/VA/VI/PA/CI/PA/L/AT/PI/EG
E/EN/LS/AA/MS/AL/LE/VO/L/PM/PI/EP/EN/EN/YS/OL/MS/KR/L/AS/AD/PI/SL/IL/HS/VE
LI/OS/IG/KR/AN/RY/VE/AT/IO/IS/AM/EL/SL/VE/PI/ST/EP/VA/VI/LI/DE/VI/SS/VE
AG/ET/ST/ET/EN/CL/EF/ST/VE/PS/PI/VE/VO/MI/PA/PI/PP/PP/KR/PI/ST/EP/VS/DO
KR/KE/VA/AC/EP/PL/HP/NS/DM/KV/VA/CP/OS/SS/MP"
variation
100..402
/anne "MIP"
/replace "c"
1869
variation
/anne "MIP"
/replace "t"
BASE COUNT 984 a 694 c 711 g 835 t
ORIGIN
Query Match 56.0%; Score 3224; Dh 9; Length 3224;
Host Local Similarity 100.0%; Prod No. 0;
Matches 3224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1. 3224
/organism "Homo sapiens"
/db_xref "taxon:9606"
/feature_type "liver"
/clone_lib "Stratagene human liver cDNA"
gene
87..2271
/anne "MIP"
87..2271
/anne "MIP"
/region_start 1
/product "microsomal triacylglyceride transfer protein"
/feature_id "AA02200.1"
/db_xref "GI:469096"
/definition "MILLAVITTE/PISSY/SAVIGNET/STANDELY/STEVILL/
DROGK/USVOPH/ISSN/VALDM/POD/DOLO/OTIM/DONNE/NOVOC/PEP/EP/
KOR/SIS/IMBEN/EL/PH/IL/LI/HR/KR/PE/SY/NA/VAL/ENI/KOL/AS/PO/L/
SS/IT/NE/VI/SGN/KV/LA/AB/KV/KR/IS/KR/AS/ST/PA/NC/VS/KR/AS/
LYR/LE/SE/VA/LA/EL/HE/NE/NE/LI/KR/IV/SK/RI/ET/EA/PI/MS/KO/AA/
I/RAV/SKY/VA/PI/VG/VE/SG/RO/OSI/ST/MS/ST/RY/OP/NI/SA/VA/SP/AF/TO
HL/KR/KE/IL/LI/KR/KE/VA/POL/VA/VA/SA/OT/SE/AL/DE/DE/SS/IL/LO/ER
FL/AC/ASH/NE/IL/KR/IS/KR/OS/OS/PI/ET/VI/IT/CT/VER/L/ON/RO/KI/KAV
VE/AR/IT/OS/PR/AR/KE/TO/PA/VI/LA/PA/NI/PEG/PL/SL/TA/EA/GE/PI/SH/AT/TA/
Q/RY/DE/PI/DE/VE/K/IN/RY/HL/NE/KR/HE/K/IV/AA/AT/IL/NN/PS/MD/KN/IL/SL/IG
L/JO/BN/KY/MI/AL/VA/UT/RI/PM/PA/RI/IV/PA/RI/PM/VA/NT/PS/SS/SA/VE/PI/EP/
PR/AS/ST/SL/IL/VS/GO/L/PR/EN/NI/FO/IG/KR/IL/OS/VA/VI/PA/CI/PA/L/AT/PI/EG
E/EN/LS/AA/MS/AL/LE/VO/L/PM/PI/EP/EN/EN/YS/OL/MS/KR/L/AS/AD/PI/SL/IL/HS/VE
LI/OS/IG/KR/AN/RY/VE/AT/IO/IS/AM/EL/SL/VE/PI/ST/EP/VA/VI/LI/DE/VI/SS/VE
AG/ET/ST/ET/EN/CL/EF/ST/VE/PS/PI/VE/VO/MI/PA/PI/PP/PP/KR/PI/ST/EP/VS/DO
KR/KE/VA/AC/EP/PL/HP/NS/DM/KV/VA/CP/OS/SS/MP"
variation
100..402
/anne "MIP"
/replace "c"
1869
variation
/anne "MIP"
/replace "t"
BASE COUNT 984 a 694 c 711 g 835 t
ORIGIN
Query Match 56.0%; Score 3224; Dh 9; Length 3224;
Host Local Similarity 100.0%; Prod No. 0;
Matches 3224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```











[illegible][illegible]

<http://life-science.gatech.edu/Gen/pep/multi.html>  
 Center: Whitehead Institute / MIT Center for  
 Center code: WILB  
 Web site: <http://www.sgc.mit.edu>  
 Contact: sequencs@alum.mit.edu  
 Project: International



This sequence was finished as follows unless otherwise indicated: all regions were double stranded, sequenced with a chemistry, or covered by high-quality data (i.e., if any attempt was made to resolve all sequencing ambiguities and repeats, all regions were covered as compressions and repeats, and the assembly was from more than one subclone, and the assembly was restriction digest).

**MAPPING INFORMATION:**  
Mapping information for this clone was provided by McPherson, Department of Genetics, Washington Univ. Mo. For additional information about the map position, see <http://www.wustl.edu/genetics>

**SOURCE INFORMATION:**  
The R62C11 human HAT library was made from the B. donor, as described by Goshima, K., Watanabe, Y., and Tatematsu, M., *Cancer Res.*, 53, 4646-4651, (1993). This approach for construction of a bacterial artificial library, Genomics 5:11-19. The clone may be obtained from Research Genetics, Inc. (<http://www.resgen.com>) or and coworkers at the Roswell Park Cancer Institute (<http://baecap.med.buffalo.edu>)

**VECTOR:** pBAC3.6

**NEIGHBORING SEQUENCES INFORMATION:**  
The clone sequenced to the left is A0001960; the clone to the right is R01-4-022. A good start of this c

localtion/guidance:  
1-204860

1. 204850 "Horned Owl" (over) 15m

/rpt_family	6.93	1.700	"r"	
/rpt_family	8.00	2.165	"M <sub>1</sub> E"	
/rpt_family	4.31	5.140	"M <sub>1</sub> E"	
/rpt_family	5.41	5.481	"l"	
/rpt_family	5.86	6.065	"M <sub>1</sub> L <sub>1</sub> B"	
/rpt_family	6.91	7.745	"M <sub>1</sub> L <sub>1</sub> B"	
/rpt_family	6.28	6.317	"l <sub>1</sub> "	
/rpt_family	7.15	7.776	"(N)"	
/rpt_family	7.805	8.438	"(A)"	
/rpt_family	8.41	8.503	"2"	
/rpt_family	8.510	9.150	"l <sub>1</sub> "	
/rpt_family	9.135	9.295	"l <sub>1</sub> "	
/rpt_family	9.568	9.988	"1,2"	
/rpt_family	9.825	9.948	"A <sub>1</sub> "	
/rpt_family	10.233	10.843	"(A)"	
/rpt_family	10.722	11.543	"A <sub>1</sub> "	
/rpt_family	11.269	11.828	"PEV"	





Gy	4197	CTTATCAAGGAAATAAATAAATTAAA	3224
Dh	7337	CGTAACAGCAAAAAAAAAAAAAAA	7364

RESULT	11
E 640-4	
LOCUS	8067 bp
DEFINITION	Sequence & from patient US 5595872.
ACCESSION	E 640-4
VERSION	1.0004
KEYWORDS	ORF1824825
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1. (bases 1 to 8067) Wetterau, J.R., II, Sharp, D.Y., Greig, R.E., Miller, S.A., Dickson, J.K., Lawrence, K. Michael, , Lawson, J.E., Holava, H.M. and Patt, Y.K.A., J.C. Nucleic acids encoding ribosomal rRNA transfer protein Patent: US 5595872 A at JAN 1997; Location/Qualifiers 1..8067 /contigism "unknown"
TITLE	/contigism "unknown"
JOURNAL	Feature
FEATURES	1..8067
SCAFFOLD	1..8067
BASE COUNT	2181 A 1555 C 1765 G 2760 T
ORIGIN	4 octets

Query Match:	16.5%;	Score 628;	DB 6;	Length 8067;
Best Local Similarity:	100.0%;	Prod. No. 0;		
Matches 628:	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

DB 5737 CAGGCAATTCAGCAAAAGCAGCAAGCGCTGTCCACAGGAGAGGTTATGTCCTCAGAA 6796  
07 2657 AAGGAAAGGAAAGCAGTATATGAGATATGTAATATGAGGTGCTGCAAGAGAAATCAATTAAT 2716

ay 2717 atctcaaatatcatatttcccccctcagccgatatactacttccacaggatctgttttggaaactq 2776

2777 **ATCTGATCTTCTGATTTCTCTCTTAAAGAGAGCAATGCTGATCAAT** 2876  
 1 |||||  
 6917 **ATCTGATCTTCTGATTTCTCTCTTAAAGAGAGCAATGCTGATCAAT** 6976

100 4997 TACTTCTCTCCAGACAGCGCTTACATATTTACCTGTATTTAGACATTTTGTAAAA 7046

2567 ctttttattatctatctatgacgctttcaagacagctttctatttacttatacctctctctca 3016

[illegible]

160 7217 AAAAAAATAAAATTAAGGACCACTTGGTTTCATTTCATTTTGAGG 7276

[illegible]

Db 7337 CCTAATCAGCAAAAAAAAAAAAAAAAA 7364

RESULT	12			
LOCUS	G19427	400 bp	JNA	Linear
DEFINITION	human STS SREG-1208, sequence tagged site.			
ACCESSION	G19427			
VERSION	G19427.1	G13244214		
KEYWORDS	STS; STS sequence; primer; sequence tagged site.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Pekaryev A, Metaxas J, Chordata: Cranial; Vertebrata: Euteleostomi; Mammalia: Eulipotyria; Primates: Catarrhini; Homioidae: Homo, 1 (bases 1 to 400)			
AUTHORS	Myers, R. M.			
JOURNAL	unpublished			
COMMENT	<p>Contact: Richard M. Myers  Stanford Human Genome Center (SHGC)  Stanford University School of Medicine  Department of Genetics, M 444, Stanford, CA 94305, USA  Tel.: 415/7259687  Fax: 415/7259689  Email: myers@shgc.stanford.edu</p>			

Primer A: GCGGAGGACGGCCTTGTGTTTC  
Primer B: GCTGTGGGTACCAATGCCA  
SIS size: 105  
PCR profile:

Denaturation:	94 degrees C for 15 seconds
Annealing:	62 degrees C for 23 seconds
Polymerization:	72 degrees C for 30 seconds

Protocol:	25 ng
Template:	each 1 μM
Primer:	each 200 μM
dNTPs:	

Sample	Temperature (°C)	Modulus (GPa)	Strain (%)	Stress (MPa)	Strain Rate (s <sup>-1</sup> )	Frequency (Hz)	Time (s)	Modulus (GPa)	Strain (%)	Stress (MPa)	Strain Rate (s <sup>-1</sup> )	Frequency (Hz)	Time (s)
Hulfer:	2.5 mm	10	10	10	10	10	10	10	10	10	10	10	10
MCH 2:	2.5 mm	10	10	10	10	10	10	10	10	10	10	10	10

pH: 8.3

Prepared with primer pairs derived from X75500 - *Utricularia* location/conditions

```

FORQUISM = "HOMO SAPIENS"
/alt_xref = "taxon:9606"
/map = "4"
79. . 183
515

```

pt and $\gamma_{\text{total}}$	comp	concentr	exp	res	err
66-28-10-0-0-0-1	1-3	a	7.2	c	64.4
66-28-10-0-0-0-1					22.9
ORIGIN					22 others

Best Local Similarity 100.0%; Prod. No. 4,20-162;  
Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2832 ctatgctatctatctcctgagagagcgtctaacctatttgcctgtatttctgaattcttg 2891

[illegible]

	RESULT	14
HSMPEP1		
LOCUS	HSMPEP1	270 bp cDNA
DEFINITION	H.sapiens MTP gene (cDNA)	
ACCESSION	X83023	
VERSION	X83023.1	GI:596800
KEYWORDS	microsomal triacylglyceride transfer protein; MTP gene	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata	
	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea	
REFERENCE	1 (bases 1 to 293)	

REFERENCE AUTHORS TITLE	JOURNAL MEDLINE AUTHORS TITLE JOURNAL	FEATURES
1 (bases 1 to 243) Sharp,D., Ricci,B., Knecht,P., Lin,M.C. and Wente Human microsomal triglyceride transfer protein car structure	Biochemistry 33 (31), 9457-9-61 (1994) 94325268 2 (bases 1 to 243) Sharp,D. Direct Submission Submitted (26-NOV-1994) Metabolic Diseases, Princeton, New Jersey 08540	location/qualifier 1...293 /organism "Homo sapiens"

FEATURES	SOURCE	LOCATION/QUALITATIVE
l_293		
organism	"Homo sapiens"	
db_xref	"taxon:9606"	
chromosome	"4"	
cell_type	"lymphocyte"	

```

intron
exon

/cstone.lib "Stratified" in "lambda.fast"
/zip-"4424"
<1..40
/number-10
41..254
/gette-"MIP"
/label-ex1
/number 11
/usedin-X8018.MIP-785

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[illegible]

DB	41	GAGTACTGGAGGCGAAGAATCTAACTCCTGAAGCTCAAAAATAAG-
QY	1491	gacaccagaaatctatcgcgtccctttaaataaacctctcttcgaagaac-



Wed Sep 18 08:38:00 2002

us-09-917-963-3.oli.rge

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Software version 4.5

September 15, 2002, 01:12:13 ; Search time 350.22 seconds  
(without alignments)  
16628.361 Million cell updates/sec

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015 09-917-9633-8
4342
1 actofctact; tprpact ..... agatagatagaaactacac 3292
Sequence
011072.NB
tadpof 60 0 , tadpox 50 0

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World sales:	0	3472872
Customer satisfaction:	0	100
Customer satisfaction chosen parameters:	0	100

Min	0.0000000000
Max	1.0000000000

Part 1: List 45 summaries

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format :
1. [S]/qdata4/hold_geneset/geneset_emb1/NA1930.DAT.*
2. [S]/qdata4/hold_geneset/geneset_emb1/NA1981.DAT.*

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11	/S1US1/arcdata/hold-geneseq/geneseqn_emb1/NA1992.DAT *
12	/S1US1/arcdata/hold-geneseq/geneseqn_emb1/NA1993.DAT *
13	/S1US1/arcdata/hold-geneseq/geneseqn_emb1/NA1994.DAT *
14	/S1US1/arcdata/hold-geneseq/geneseqn_emb1/NA1995.DAT *
15	/S1US1/arcdata/hold-geneseq/geneseqn_emb1/NA1996.DAT *
16	/S1US1/arcdata/hold-geneseq/geneseqn_emb1/NA1997.DAT *
17	/S1US1/arcdata/hold-geneseq/geneseqn_emb1/NA1998.DAT *
18	/S1US1/arcdata/hold-geneseq/geneseqn_emb1/NA1999.DAT *
19	/S1US1/arcdata/hold-geneseq/geneseqn_emb1/NA2000.DAT *
20	/S1US1/arcdata/hold-geneseq/geneseqn_emb1/NA2001.DAT *
21	/S1US1/arcdata/hold-geneseq/geneseqn_emb1/NA2002.DAT *
22	/S1US1/arcdata/hold-geneseq/geneseqn_emb1/NA2003.DAT *
23	/S1US1/arcdata/hold-geneseq/geneseqn_emb1/NA2004.DAT *
24	/S1US1/arcdata/hold-geneseq/geneseqn_emb1/NA2005.DAT *

## SUMMARY

Result No.	Score	X		Length (kb)	ID	Description
		Match	Ident			
1	4144	92.4	3185	14	AA050430	Human MTP, Homo S
2	4377	17.0	8668	14	AA050433	Partial human geno
3	174	12.4	1221	22	AA033669	Human colon cancer
4	174	5.1	1245	21	AA0307327	Human secreted pro
5	103	4.0	402	14	AA050446	MTP exon 13 mutant
6	76	2.2	107	14	AA050431	bovine MTP 5' end,
7	51	1.5	51	22	AAH79978	Human DNA containi
8	46	1.4	2900	14	AA050429	Human MTP, Bos t
9	43	1.0	43	14	AA050443	bovine MTP, Bos t MTP (265-287) norm

[illegible]











of cholesterol ester in a mammalian species.  
 CC Diseases associated or affected by serum lipid levels, such as  
 CC fatty aciditis, hypertriglyceridemia, obesity, etc., may be treated.  
 CC  
 CC Sequence 102 BP: 76 A; 67 C; 55 G; 104 T; 0 other:

Query Match 4.0%; Score 103; DB 14; Length 302;

Best Local Similarity 100.0%; Prod. No. 9-2e-28;  
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YY 1954 apaaatattgtctgtatatttataaataatgtctgtatattatgaacattttctc 1913  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 104 apaaatattgtctgtatatttataaataatgtctgtatattatgaacattttctc 163

YY 1914 apaaatattgtctgtatatttataaataatgtctgtatattatgaacattttctc 1956  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 164 apaaatattgtctgtatatttataaataatgtctgtatattatgaacattttctc 206

# RESULT 6

AA050431

DB AA050431 standard: cDNA; 107 BP

XX AA050431

XX 10 MAY-1994 (first entry)

XX 10 MAY-1994 (first entry)

XX 10 MAY-1994 (first entry)

XX 10 MAY-1994 (first entry)

XX 10 MAY-1994 (first entry)

XX 10 MAY-1994 (first entry)

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XX 10 MAY-1994 (first entry)

XX 10 MAY-1994 (first entry)

XX 10 MAY-1994 (first entry)

XX 10 MAY-1994 (first entry)

XX 10 MAY-1994 (first entry)

CC Bovine and human MTP are useful for the prevention, stab-  
 CC repression of atherosclerosis or for lowering the level  
 CC lipids such as serum cholesterol, triglyceride, phosphati-  
 CC or cholesterol ester in a mammalian species.  
 CC Diseases associated or affected by serum lipid levels, s-  
 CC pancreaticitis, hypertriglyceridemia, obesity, etc., may be treated.  
 CC  
 CC Sequence 107 BP: 40 A; 28 C; 11 G; 0 other:

Query Match 2.2%; Score 74; DB 14; Length 1

Best Local Similarity 100.0%; Prod. No. 6e-18;  
 Matches 76; Conservative 0; Mismatches 0; Indels 0;

YY 106 tttctctgtctatatttataaataatgtctgtatattatgaacattttctc 1913  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 1 tttctctgtctatatttataaataatgtctgtatattatgaacattttctc 163

YY 166 catataataatgaacattttctc 181

DB 61 catataataatgaacattttctc 76

# RESULT 7

AAH79978

DB AAH79978 standard: DNA; 51 BP

XX AAH79978

XX 19 SEP-2001 (first entry)

XX 19 SEP-2001 (first entry)

XX 19 SEP-2001 (first entry)

XX 19 SEP-2001 (first entry)

XX 19 SEP-2001 (first entry)

XX 19 SEP-2001 (first entry)

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XX 19 SEP-2001 (first entry)

XX 19 SEP-2001 (first entry)

XX 19 SEP-2001 (first entry)

XX 19 SEP-2001 (first entry)

XX 19 SEP-2001 (first entry)

CC Bovine and human MTP are useful for the prevention, stab-  
 CC repression of atherosclerosis or for lowering the level  
 CC lipids such as serum cholesterol, triglyceride, phosphati-  
 CC or cholesterol ester in a mammalian species.  
 CC Diseases associated or affected by serum lipid levels, s-  
 CC pancreaticitis, hypertriglyceridemia, obesity, etc., may be treated.  
 CC  
 CC Sequence 107 BP: 40 A; 28 C; 11 G; 0 other:

Query Match 2.2%; Score 74; DB 14; Length 1

Best Local Similarity 100.0%; Prod. No. 6e-18;  
 Matches 76; Conservative 0; Mismatches 0; Indels 0;

YY 106 tttctctgtctatatttataaataatgtctgtatattatgaacattttctc 1913  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 1 tttctctgtctatatttataaataatgtctgtatattatgaacattttctc 163

YY 166 catataataatgaacattttctc 181

DB 61 catataataatgaacattttctc 76

# RESULT 7

AAH79978

DB AAH79978 standard: DNA; 51 BP

XX AAH79978

XX 19 SEP-2001 (first entry)

XX 19 SEP-2001 (first entry)

XX 19 SEP-2001 (first entry)

XX 19 SEP-2001 (first entry)

XX 19 SEP-2001 (first entry)

XX 19 SEP-2001 (first entry)

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XX 19 SEP-2001 (first entry)

XX 19 SEP-2001 (first entry)

XX 19 SEP-2001 (first entry)

XX 19 SEP-2001 (first entry)

XX 19 SEP-2001 (first entry)

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XX 19 SEP-2001 (first entry)

XX 19 SEP-2001 (first entry)

XX 19 SEP-2001 (first entry)

XX 19 SEP-2001 (first entry)

used in gene/ethnic therapy studies; modulation of the expression and activity of proteins related to angiogenesis, 4-hydroxyphenylpyruvate decarboxylase, adenosine triphosphate (ATP) class I histocompatibility antigen major histocompatibility complex (MHC) class I histocompatibility antigen and/or phosphatidylesterase; disorders that may be prevented, diagnosed and/or treated by the above methods include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g., rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Crohn's disease), inflammation, cancer (e.g., cancers of the bladder, brain, breast, colon and kidney, leukemia), diseases of the nervous system, an infection of pathogenic organisms. They may also be used to alter phenotypic traits such as longevity, fecundity, strength, speed and endurance.

Sequence 51 bp: 15 A; 13 C; 9 G; 14 T; 0 other;

Query Match 1.58; Score 51; DB 22; Length 51;  
Best Local Similarity 100.0%; Pred. No. 7; Le-09;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1816 ccattatcaagacatctacttgaatgctgcgaacgaattgtcc 1866  
|||||  
ID 1 ccattatcaagacatctacttgaatgctgcgaacgaattgtcc 51

RESULT: 4  
AA050429  
11 AA050429 standard; cDNA; 2900 bp;

XX  
AC AA050429;

XX  
UT 10-MAY-1994 (first entry)

XX  
DE bovine MTP.

XX  
KW MTP: microsomal triacylglyceride transfer protein; obesity;

XX  
KW atherosclerosis; detection; inhibitor; prevention; stabilisation;

XX  
KW phosphatidyl lipid; serum cholesterol; TG; triacylglyceride; TG;

XX  
KW phosphatidyl choline; pc; cholesterol; ester; CE;

XX  
KW pancreatic; hyperglycemia; ss;

XX  
OS homo sapiens;

XX  
EH Key Location/Qualifiers

XX  
F1 CDS 1..2583

XX  
F1 /\*tag a

XX  
F1 /product MTP

XX  
F1 5'UTR 2584..2881

XX  
F1 /\*tag b

XX  
F1 3'UTR 2882..2900

XX  
F1 /\*tag c

XX  
F1

XX  
F1

XX  
F1

XX  
F1

XX  
F1

XX  
F1

XX  
F1

XX  
F1

claim 3 4, page 34 17, 112pp, English.

XX  
CC the sequences given in AA050429 34 may be used for the detection of MTP or MTP inhibitors.

XX  
CC bovine and human MTP are useful for the prevention, stabilisation or regression of atherosclerosis or for lowering the level of serum lipids such as serum cholesterol, triacylglyceride, phosphatidyl choline or cholesteryl ester in a mammalian species.

XX  
CC diseases associated or affected by serum lipids, lipids, such as pancreatitis, hyperglycemia, obesity, etc., may be treated.

XX  
CC

QY Sequence 2900 bp: 890 A; 627 T; 618 G; 745 C; 0 other;

Query Match 1.48; Score 48; DB 14; Length 2900;  
Best Local Similarity 100.0%; Pred. No. 4; 3e-08;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 927 gattcaaaagacacagcattccattgtgagacagatcttccagagc 974  
|||||  
ID 739 gattcaaaagacacagcattccattgtgagacagatcttccagagc 786

RESULT: 9

AA050443  
1D AA050443 standard; cDNA; 43 bp;

XX  
AC AA050443;

XX  
UT 10-MAY-1994 (first entry)

XX  
DE MTP (255-287) normal.

XX  
KW MTP: microsomal triacylglyceride transfer protein; obesity;

XX  
KW atherosclerosis; detection; inhibitor; prevention; stabilisation;

XX  
KW phosphatidyl lipid; serum cholesterol; TG; triacylglyceride; TG;

XX  
KW phosphatidyl choline; pc; cholesterol; ester; CE;

XX  
KW pancreatic; hyperglycemia; abetalipoproteinemia; amplification;

XX  
KW primer; polynucleotide chain reaction; PCR; ss;

XX  
OS homo sapiens;

XX  
EH Key Location/Qualifiers

XX  
F1 mutation 8

XX  
F1 /\*tag a

XX  
F1 /note "cytosine deleted in Abeta"

XX  
F1

XX  
F1

XX  
F1

XX  
F1

XX  
F1

XX  
F1

XX  
F1

XX  
F1

XX  
F1

XX  
F1

XX  
F1

XX  
F1

Disclosure: page 68; 112pp; English.

XX  
CC The primers given in AA050443-42 and AA050444-45 are based on the normal human cDNA encoding the 84 kD component of MTP. The primers were used in the detection of a gene defect in an abetalipoproteinemic subject (intestinal biopsy).



```

ER 08-NOV-2000; 2000008-0246542.
PK 08-NOV-2000; 2000008-0246609.
PK 08-NOV-2000; 2000008-0246610.
PK 08-NOV-2000; 2000008-0246611.
PK 08-NOV-2000; 2000008-0246612.
PK 17-NOV-2000; 2000008-0249205.
PK 17-NOV-2000; 2000008-0249206.
PK 17-NOV-2000; 2000008-0249207.
PK 17-NOV-2000; 2000008-0249208.
PK 17-NOV-2000; 2000008-0249209.
PK 17-NOV-2000; 2000008-0249210.
PK 17-NOV-2000; 2000008-0249211.
PK 17-NOV-2000; 2000008-0249212.
PK 17-NOV-2000; 2000008-0249213.
PK 17-NOV-2000; 2000008-0249214.
PK 17-NOV-2000; 2000008-0249215.
PK 17-NOV-2000; 2000008-0249216.
PK 17-NOV-2000; 2000008-0249217.
PK 17-NOV-2000; 2000008-0249218.
PK 17-NOV-2000; 2000008-0249244.
PK 17-NOV-2000; 2000008-0249245.
PK 17-NOV-2000; 2000008-0249246.
PK 17-NOV-2000; 2000008-0249247.
PK 17-NOV-2000; 2000008-0249248.
PK 17-NOV-2000; 2000008-0249249.
PK 17-NOV-2000; 2000008-0249250.
PK 01-DEC-2000; 2000008-0250163.
PK 01-DEC-2000; 2000008-0250164.
PK 05-DEC-2000; 2000008-0250180.
PK 05-DEC-2000; 2000008-0251984.
PK 05-DEC-2000; 2000008-0256719.
PK 06-DEC-2000; 2000008-0251479.
PK 08-DEC-2000; 2000008-0251876.
PK 08-DEC-2000; 2000008-0251884.
PK 08-DEC-2000; 2000008-0251885.
PK 08-DEC-2000; 2000008-0251989.
PK 08-DEC-2000; 2000008-0251990.
PK 11-DEC-2000; 2000008-0254097.
PK 05-JAN-2001; 2000008-0254670.
XX
XX
XX (HUMA-) HUMAN GIMME SET 1N*.
XX
XX Rosen CA, Barash SC, Folini SM:
XX WPI: 2001-465570750.
XX
XX
XX Isolated nucleic acid molecule encoding a reproductive system antigen
XX is used in preventing, treating or ameliorating a medical condition.
XX
XX Disclosure: SEQ ID NO 7631: 1297bp + sequence listing; English.
XX
XX The present invention provides a protein and coding sequences of a
XX number of human reproductive system related antigens. These can be used
XX in the prevention and treatment of reproductive system disorders,
XX including cancer. The present sequence is a genomic sequence encoding a
XX protein of the invention.
XX
XX Sequence 9741 BP: 2959 A; 1576 C; 1920 G; 4275 T; 1 other:
XX
Query Match 0.98; Score 29; 198 22; Length 9741;
Host Local Similarity 100.0%; Prod. No. 0.25;
Mat Desc 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 4204 AAAAAAAAAAAAAAAAAAATGAAA 3232
XX TTTTTTTTTTTTTTTTTTTTTTTTTT
XX 2679 AAAAAAAAAAAAAAAAAAATGAAA 2671
XX
XX
XX RESULT 11
XX AA255247
XX ID AA255247 standard; cDNA; 114 BP.
XX
XX AA255247
XX

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PT 06-OCT-2000 (first entry)
XX
XX Human secreted protein 5' EST, SPO ID NO: 29598.
XX
XX Human 5' EST, expressed sequence tag, secreted protein, cDNA isolated from
XX gene therapy; chromosome mapping; ss.
XX
XX Homo sapiens.
XX
XX EP103401-A2.
XX
XX 06 SEP 2000.
XX
XX 21-SEP-2000; 2000EP-0200610.
XX
XX 26 FEB 1999, 9903 0122487.
XX
XX (GEST ) GENSET.
XX
XX Dumas Milne Edwards J, Duret A, Giordano J:
XX WPI: 2000-500381/45.
XX
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures
XX
XX Claim 1: SEQ ID 29598; 71bp + CD-ROM; English.
XX
XX
XX The present sequence is one of a large number of 5' ESTs derived from
XX cDNAs encoding secreted proteins. No gap has yet been conclusively
XX identified within the present sequence. The 5' ESTs were prepared from
XX total human RNAs or poly(A) RNAs derived from 49 different tissues. EST
XX sequences usually correspond mainly to the 4' untranslated region (UTR)
XX of the mRNA because they are often obtained from oligo-dT primed cDNA
XX libraries. Such ESTs are not well suited for isolating cDNA sequences
XX derived from the 5' ends of mRNAs and even in those cases where longer
XX cDNA sequences have been obtained, the full 5' UTR is rarely included.
XX 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
XX used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
XX in diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX They are used to obtain upstream regulatory sequences and to design
XX expression and secretion vectors.
XX
XX Sequence 114 BP: 40 A; 11 C; 17 G; 46 T; 0 other:
XX
Query Match 0.89; Score 27; 198 21; Length 114;
Host Local Similarity 100.0%; Prod. No. 2.87;
Mat Desc 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 3207 AAAAAAAAAAAAAAAAAAATGAAA 3233
XX TTTTTTTTTTTTTTTTTTTTTTTTTT
XX 114 AAAAAAAAAAAAAAAAAAATGAAA 88
XX
XX
XX RESULT 12
XX AAH71501
XX ID AAH71501 standard; cDNA; 203 BP.
XX
XX AAH71501;
XX
XX 19 SEP 2001 (first entry)
XX
XX Human cervical cancer marker nucleic acid 2775.
XX
XX Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX
XX Homo sapiens.
XX
XX W9290142467-A2
XX
XX 14-JUN-2001.
XX

```

XX 908 (b) 2000: 2000W-0533312.  
 XX 08 (b) 1999: 9908-0169681.  
 XX 21 (b) 1999: 9908-0171450.  
 XX 14 MAY 2000: 200008-0189415.  
 XX 12 MAY 2000: 200008-0204791.  
 XX 09 JUN 2000: 200008-0210600.  
 XX 21 JUN 2000: 200008-0220114.  
 XX (MILL.) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX Schlegel R., Woods J., Berger A., Zhao X.  
 XX WPI: 2001-375006/39.  
 XX New isolated nucleic acid for diagnosing and treating cervical cancer  
 XX and for assessing and detecting compounds for treating the cancer -  
 XX Claim 1: Page 570; 1051pp; English.  
 XX The invention relates to novel genes (AAH68727-AAH73382) associated with  
 XX cervical cancer with cytostatic activity. The nucleic acids and encoded  
 XX polypeptides are useful to assess if a patient is afflicted with  
 XX cervical cancer or has a pre-malignant condition to monitor the  
 XX progression of cervical cancer or a pre-malignant condition in a patient;  
 XX and to select and/or assess the efficacy of a compound or therapy for  
 XX inhibiting cervical cancer in a patient. The nucleic acids may also be  
 XX useful for gene therapy.  
 XX Sequence 204 BP; 91 A; 25 C; 29 G; 58 T; 0 other;

Query Match 0.88; Score 27; 28 22; Length 203;  
 Best Local Similarity 100.0%; Pred. No. 2.5;  
 Matches 27; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

G7 3290 aatcagagaaaaaaatcagagaaaaaa 3225  
 1b 145 aatcagagaaaaaaatcagagaaaaaa 169

## RESULT 13

AAH70076 standard: cDNA; 225 BP.

AAH70076:

19 SEP 2001 (first entry)

human cervical cancer marker nucleic acid 1350.

cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.

human sapiens.

W2000142467-A2.

14 JUN 2001.

08 (b) 2000: 2000W-0533312.

08 (b) 1999: 9908-0169681.

21 (b) 1999: 9908-0171450.

14 MAY 2000: 200008-0189415.

12 MAY 2000: 200008-0204791.

09 JUN 2000: 200008-0210600.

21 JUN 2000: 200008-0220114.

(MILL.) MILLENNIUM PREDICTIVE MEDICINE INC.

Schlegel R., Woods J., Berger A., Zhao X.

DR WPI: 2001-375006/39.  
 XX New isolated nucleic acid for diagnosing and treating cervical  
 XX cancer and for assessing and detecting compounds for treating the  
 XX Claim 1: Page 313; 1051pp; English.  
 XX The invention relates to novel genes (AAH68727-AAH73382) a  
 XX cervical cancer with cytostatic activity. The nucleic acids  
 XX polypeptides are useful to assess if a patient is afflicted  
 XX cervical cancer or has a pre-malignant condition to monitor the  
 XX progression of cervical cancer or a pre-malignant condition  
 XX and to select and/or assess the efficacy of a compound or  
 XX inhibiting cervical cancer in a patient. The nucleic acids  
 XX useful for gene therapy.  
 XX Sequence 225 BP; 92 A; 33 C; 37 G; 10 T; 1 other;

Query Match 0.88; Score 27; 28 22; Length 225;  
 Best Local Similarity 100.0%; Pred. No. 2.5;  
 Matches 27; Conservative 9; Mismatches 0; Indels 0;

G7 3290 aatcagagaaaaaaatcagagaaaaaa 3225  
 1b 165 aatcagagaaaaaaatcagagaaaaaa 169

## RESULT 14

AA224427

AA224427 standard: cDNA; 925 BP.

AA224427:

14-FEB-2000 (first entry)

Human bladder tumour cDNA library derived EST 49

Expressed sequence tag; human; bladder tumour; cDNA; EST

treatment; gene therapy; EST; ss.

human sapiens.

DE19818619-A1.

28-OCT-1999.

21-APR-1998; 98DE-1018619.

21-APR-1998; 98DE-1018619.

(META-) METACEN GDS GINOM74833 (HNF 1B).

Rosenblatt A., Specht T., Hinzmann A., Schmitt A., Lissack

WPI: 1999-612029/53.

New nucleic acid sequences expressed in bladder tumor cells

derived polypeptides, for treatment of bladder tumor and

of therapeutic agents

Claim 3: Page 90; 132pp; German.

This invention describes novel polypeptide treatments (1)

polynucleotides (11) that encode them that are highly effective

human bladder tumour and which have cytostatic activity.

for recombinant expression of (1) and to isolate compounds

used to identify agents suitable for treatment of bladder

cervical cancer or has a pre-malignant condition to monitor the

progression of cervical cancer or a pre-malignant condition

and to select and/or assess the efficacy of a compound or

inhibiting cervical cancer in a patient. The nucleic acids

useful for gene therapy.

Sequence 225 BP; 92 A; 33 C; 37 G; 10 T; 1 other;





...